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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/888,320

DATE: 02/21/2002  
 TIME: 12:01:24

Input Set : A:\Nih413-1.app  
 Output Set: N:\CRF3\02212002\I888320.raw

Does Not Comply  
 Corrected Diskette Needed  
*x and*

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3 <110> APPLICANT: Barry III, Clifton E.
4 DeBarber, Andrea E.
5 Mdluli, Khisimuzi
6 Bekker, Linda-Gail
7 The Government of the United States of America
8 as represented by The Secretary of the
9 Department of Health and Human Services
11 <120> TITLE OF INVENTION: Methods of Diagnosing Multidrug Resistant Tuberculosis
13 <130> FILE REFERENCE: 015280-413100US
15 <140> CURRENT APPLICATION NUMBER: US 09/888,320
16 <141> CURRENT FILING DATE: 2001-06-22
18 <150> PRIOR APPLICATION NUMBER: US 60/214,187
19 <151> PRIOR FILING DATE: 2000-06-26
21 <160> NUMBER OF SEQ ID NOS: 16
23 <170> SOFTWARE: PatentIn Ver. 2.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1867
27 <212> TYPE: DNA
28 <213> ORGANISM: Mycobacterium tuberculosis
30 <220> FEATURE:
31 <223> OTHER INFORMATION: wild-type EtaA monooxygenase (Rv3854c, EthA)
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (201)..(1670)
36 <223> OTHER INFORMATION: EtaA
38 <400> SEQUENCE: 1
39 agcggacggt cctcgagaag gttctcggcg gtggcgagga tcgccagttc acgategctg 60
41 ccggacggcc gcgcggtgcy ccggcccta ggcagcgaa cctgactggc cgcggaggtg 120
43 gtacacctgg cagcttacta cgtgtcgata gtgtogacat ctggttgacg gcctcgacat 180
45 tacgttgata gcgtggatcc atg acc gag cac ctc gac gtt gtc atc gtg ggc 233
46 Met Thr Glu His Leu Asp Val Val Ile Val Gly
47 1 5 10
49 gct gga atc tcc ggt gtc agc gcg gcc tgg cac ctg cag gac cgt tgc 281
50 Ala Gly Ile Ser Gly Val Ser Ala Ala Trp His Leu Gln Asp Arg Cys
51 15 20 25
53 ccg acc aag agc tac gcc atc ctg gaa aag cgg gaa tcc atg ggc ggc 329
54 Pro Thr Lys Ser Tyr Ala Ile Leu Glu Lys Arg Glu Ser Met Gly Gly
55 30 35 40
57 acc tgg gat ttg ttc cgt tat ccc gga att cgc tcc gac tcc gac atg 377
58 Thr Trp Asp Leu Phe Arg Tyr Pro Gly Ile Arg Ser Asp Ser Asp Met
59 45 50 55
61 tac acg cta ggt ttc cga ttc cgt ccc tgg acc gga cgg cag gcg atc 425
62 Tyr Thr Leu Gly Phe Arg Phe Arg Pro Trp Thr Gly Arg Gln Ala Ile

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63	60			65		70		75	
65	gcc	gac	ggc	aag	ccc	atc	ctc	gag	tac
66	Ala	Asp	Gly	Lys	Pro	Ile	Leu	Glu	Tyr
67				80				85	
69	tat	gga	atc	gac	agg	cat	atc	cgg	ttc
70	Tyr	Gly	Ile	Asp	Arg	His	Ile	Arg	Phe
71				95				100	
73	gat	tgg	tcg	acc	ggc	gaa	aac	cgc	tgg
74	Asp	Trp	Ser	Thr	Ala	Glu	Asn	Arg	Trp
75				110				115	
77	ggc	acg	ctc	agc	gcc	ctc	acc	tgc	gaa
78	Gly	Thr	Leu	Ser	Ala	Leu	Thr	Cys	Glu
79				125				130	
81	tac	tac	aac	tac	gac	gag	ggc	tac	tcg
82	Tyr	Tyr	Asn	Tyr	Asp	Glu	Gly	Tyr	Ser
83	140							145	
85	gat	ttc	gtc	ggg	ccg	atc	atc	cat	ccg
86	Asp	Phe	Val	Gly	Pro	Ile	Ile	His	Pro
87								160	
89	gac	tac	gac	gct	aag	aac	atc	gtc	gtg
90	Asp	Tyr	Asp	Ala	Lys	Asn	Ile	Val	Val
91				175				180	
93	gtc	acg	ctc	gtg	ccg	ggc	ctg	ggc	gac
94	Val	Thr	Leu	Val	Pro	Ala	Leu	Ala	Asp
95				190				195	
97	atg	ctg	cag	cgc	tca	ccc	acc	tac	atc
98	Met	Leu	Gln	Arg	Ser	Pro	Thr	Tyr	Ile
99				205				210	
101	ggc	atc	gcc	gag	aag	ctc	aac	cgc	tgg
102	Gly	Ile	Ala	Glu	Lys	Leu	Asn	Arg	Trp
103	220							225	
105	acc	ggc	gta	cgg	tgg	aag	aac	gtg	ctg
106	Thr	Ala	Val	Arg	Trp	Lys	Asn	Val	Leu
107				240				245	
109	gcc	tgc	cag	aag	tgg	cca	cgg	cgc	atg
110	Ala	Cys	Gln	Lys	Trp	Pro	Arg	Arg	Met
111				255				260	
113	atc	cag	cgc	cag	cta	ccc	gag	ggg	tac
114	Ile	Gln	Arg	Gln	Leu	Pro	Glu	Gly	Tyr
115				270				275	
117	ccg	cac	tac	aac	ccc	tgg	gac	cag	cga
118	Pro	His	Tyr	Asn	Pro	Trp	Asp	Gln	Arg
119				285				290	
121	gac	ctg	ttc	cgg	gcc	att	cgt	cac	ggg
122	Asp	Leu	Phe	Arg	Ala	Ile	Arg	His	Gly
123	300							305	
125	acc	att	gaa	cgg	ttc	acc	ggc	acc	gga
126	Thr	Ile	Glu	Arg	Phe	Thr	Ala	Thr	Gly
127								320	
								325	
								330	

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129 gaa ctg ccg gct gac atc atc att acc gca acg ggg ttg aac ctg cag 1241
130 Glu Leu Pro Ala Asp Ile Ile Ile Thr Ala Thr Gly Leu Asn Leu Gln
131 335 340 345
133 ctt ttt ggt ggg gcg acg gcg act atc gac gga caa caa gtg gac atc. 1289
134 Leu Phe Gly Gly Ala Thr Ala Thr Ile Asp Gly Gln Gln Val Asp Ile
135 350 355 360
137 acc acg acg atg gcc tac aag ggc atg atg ctt tcc ggc atc ccc aac 1337
138 Thr Thr Thr Met Ala Tyr Lys Gly Met Met Leu Ser Gly Ile Pro Asn
139 365 370 375
141 atg gcc tac acg gtt ggc tac acc aat gcc tcc tgg acg ctg aag gcc 1385
142 Met Ala Tyr Thr Val Gly Tyr Thr Asn Ala Ser Trp Thr Leu Lys Ala
143 380 385 390 395
145 gac ctg gtg tgc gag ttt gtc tgt cgc ttg ttg aat tac atg gac gac 1433
146 Asp Leu Val Ser Glu Phe Val Cys Arg Leu Leu Asn Tyr Met Asp Asp
147 400 405 410
149 aac ggt ttt gac acc gtg gtc gtc gag cga cgc ggc tca gat gtc gaa 1481
150 Asn Gly Phe Asp Thr Val Val Val Glu Arg Pro Gly Ser Asp Val Glu
151 415 420 425
153 gag cgg ccc ttc atg gag ttc acc cca ggt tac gtg ctg cgc tgc ctg 1529
154 Glu Arg Pro Phe Met Glu Phe Thr Pro Gly Tyr Val Leu Arg Ser Leu
155 430 435 440
157 gac gag ctg ccc aag cag ggt tgc cgt aca cgc tgg cgc ctg aat cag 1577
158 Asp Glu Leu Pro Lys Gln Gly Ser Arg Thr Pro Trp Arg Leu Asn Gln
159 445 450 455
161 aac tac cta cgt gac atc cgg ctc atc cgg cgc ggc aag atc gac gac 1625
162 Asn Tyr Leu Arg Asp Ile Arg Leu Ile Arg Arg Gly Lys Ile Asp Asp
163 460 465 470 475
165 gag ggt ctg cgg ttc gcc aaa agg cct gcc cgc gtg ggg gtt tag 1670
166 Glu Gly Leu Arg Phe Ala Lys Arg Pro Ala Pro Val Gly Val
W--> 167 480 485 490
169 ctttagcgac gggttagcgc cgggttaggc catagtcaga cgacgatgat gccgtcgtcg 1730
171 tgcgtgttag cgatatcgcc cggaacgaat gtacccccgc ccagcgtgat ttcaacgtcg 1790
173 cggttctcgg caccggtctt ggtgctcttg cggggattgg tgcccagcgc ttgatgcgc 1850
175 atgtcgatgc cgcgcag
178 <210> SEQ ID NO: 2
179 <211> LENGTH: 489
180 <212> TYPE: PRT
181 <213> ORGANISM: Mycobacterium tuberculosis } <220>
182 <223> OTHER INFORMATION: wild-type EtAa monoxygenase (Rv3854c, EthA)
184 <400> SEQUENCE: 2
185 Met Thr Glu His Leu Asp Val Val Ile Val Gly Ala Gly Ile Ser Gly
186 1 5 10 15
187 Val Ser Ala Ala Trp His Leu Gln Asp Arg Cys Pro Thr Lys Ser Tyr
188 20 25 30
189 Ala Ile Leu Glu Lys Arg Glu Ser Met Gly Gly Thr Trp Asp Leu Phe
190 35 40 45
191 Arg Tyr Pro Gly Ile Arg Ser Asp Ser Asp Met Tyr Thr Leu Gly Phe
192 50 55 60
193 Arg Phe Arg Pro Trp Thr Gly Arg Gln Ala Ile Ala Asp Gly Lys Pro

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```

194 65              70              75              80
195 Ile Leu Glu Tyr Val Lys Ser Thr Ala Ala Met Tyr Gly Ile Asp Arg
196              85              90              95
197 His Ile Arg Phe His His Lys Val Ile Ser Ala Asp Trp Ser Thr Ala
198              100              105              110
199 Glu Asn Arg Trp Thr Val His Ile Gln Ser His Gly Thr Leu Ser Ala
200              115              120              125
201 Leu Thr Cys Glu Phe Leu Phe Leu Cys Ser Gly Tyr Tyr Asn Tyr Asp
202              130              135              140
203 Glu Gly Tyr Ser Pro Arg Phe Ala Gly Ser Glu Asp Phe Val Gly Pro
204 145              150              155              160
205 Ile Ile His Pro Gln His Trp Pro Glu Asp Leu Asp Tyr Asp Ala Lys
206              165              170              175
207 Asn Ile Val Val Ile Gly Ser Gly Ala Thr Ala Val Thr Leu Val Pro
208              180              185              190
209 Ala Leu Ala Asp Ser Gly Ala Lys His Val Thr Met Leu Gln Arg Ser
210              195              200              205
211 Pro Thr Tyr Ile Val Ser Gln Pro Asp Arg Asp Gly Ile Ala Glu Lys
212              210              215              220
213 Leu Asn Arg Trp Leu Pro Glu Thr Met Ala Tyr Thr Ala Val Arg Trp
214 225              230              235              240
215 Lys Asn Val Leu Arg Gln Ala Ala Val Tyr Ser Ala Cys Gln Lys Trp
216              245              250              255
217 Pro Arg Arg Met Arg Lys Met Phe Leu Ser Leu Ile Gln Arg Gln Leu
218              260              265              270
219 Pro Glu Gly Tyr Asp Val Arg Lys His Phe Gly Pro His Tyr Asn Pro
220              275              280              285
221 Trp Asp Gln Arg Leu Cys Leu Val Pro Asn Gly Asp Leu Phe Arg Ala
222              290              295              300
223 Ile Arg His Gly Lys Val Glu Val Val Thr Asp Thr Ile Glu Arg Phe
224 305              310              315              320
225 Thr Ala Thr Gly Ile Arg Leu Asn Ser Gly Arg Glu Leu Pro Ala Asp
226              325              330              335
227 Ile Ile Ile Thr Ala Thr Gly Leu Asn Leu Gln Leu Phe Gly Gly Ala
228              340              345              350
229 Thr Ala Thr Ile Asp Gly Gln Gln Val Asp Ile Thr Thr Thr Met Ala
230              355              360              365
231 Tyr Lys Gly Met Met Leu Ser Gly Ile Pro Asn Met Ala Tyr Thr Val
232              370              375              380
233 Gly Tyr Thr Asn Ala Ser Trp Thr Leu Lys Ala Asp Leu Val Ser Glu
234 385              390              395              400
235 Phe Val Cys Arg Leu Leu Asn Tyr Met Asp Asp Asn Gly Phe Asp Thr
236              405              410              415
237 Val Val Val Glu Arg Pro Gly Ser Asp Val Glu Glu Arg Pro Phe Met
238              420              425              430
239 Glu Phe Thr Pro Gly Tyr Val Leu Arg Ser Leu Asp Glu Leu Pro Lys
240              435              440              445
241 Gln Gly Ser Arg Thr Pro Trp Arg Leu Asn Gln Asn Tyr Leu Arg Asp
242              450              455              460

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```

243 Ile Arg Leu Ile Arg Arg Gly Lys Ile Asp Asp Glu Gly Leu Arg Phe
244 465                               470                               475                               480
245 Ala Lys Arg Pro Ala Pro Val Gly Val
246                               485
250 <210> SEQ ID NO: 3
251 <211> LENGTH: 30
252 <212> TYPE: DNA
253 <213> ORGANISM: Artificial Sequence
255 <220> FEATURE:
256 <223> OTHER INFORMATION: Description of Artificial Sequence:EtaA PCR
257   amplification primer
259 <400> SEQUENCE: 3
260 ggggtaccga cattacgttg atagcgtgga                               30
263 <210> SEQ ID NO: 4
264 <211> LENGTH: 37
265 <212> TYPE: DNA
266 <213> ORGANISM: Artificial Sequence
268 <220> FEATURE:
269 <223> OTHER INFORMATION: Description of Artificial Sequence:EtaA PCR
270   amplification primer
272 <400> SEQUENCE: 4
273 ataagaatgc ggcgcgaacc gtcgctaaag ctaaacc                               37
276 <210> SEQ ID NO: 5
277 <211> LENGTH: 18
278 <212> TYPE: DNA
279 <213> ORGANISM: Artificial Sequence
281 <220> FEATURE:
282 <223> OTHER INFORMATION: Description of Artificial Sequence:EtaA Primer 3
283   sequencing primer, EtaA amplification primer
285 <400> SEQUENCE: 5
286 atcatccatc cgcagcac                               18
289 <210> SEQ ID NO: 6
290 <211> LENGTH: 17
291 <212> TYPE: DNA
292 <213> ORGANISM: Artificial Sequence
294 <220> FEATURE:
295 <223> OTHER INFORMATION: Description of Artificial Sequence:EtaA Primer 3
296   sequencing primer, EtaA amplification primer
298 <400> SEQUENCE: 6
299 aagctgcagg ttcaacc                               17
302 <210> SEQ ID NO: 7
303 <211> LENGTH: 17
304 <212> TYPE: DNA
305 <213> ORGANISM: Artificial Sequence
307 <220> FEATURE:
308 <223> OTHER INFORMATION: Description of Artificial Sequence:EtaA Primer 3
309   sequencing primer, EtaA amplification primer
311 <400> SEQUENCE: 7
312 gcatcgtgac gtgcttg                               17

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/888,320

DATE: 02/21/2002

TIME: 12:01:25

Input Set : A:\Nih413-1.app

Output Set: N:\CRF3\02212002\I888320.raw

L:167 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1